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Result
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Maximum
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Q9DXF1
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               Q9h8i7 homo sapien
Q9d4f1 mus musculu
Q9uxt5 pyrococcus
Q9xux9 caenorhabdi
Q97kl3 clostridium
Q95kk4 oryctolagus
Q8r2k3 mus musculu
Q9cyr0 mus musculu
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Q16583 caenorhabdi
Q98qa6 mycoplasma
Q92dq9 listeria in
Q8y8y2 listeria mo
Q48599 lactococcus
Q48599 lactococcus
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ALIGNMENTS

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RESULT 1
Q9H817
Q9H817
Q9H817
Q9H818
AC Q9H8
AC Q1-M
AC CDNA
OC Euka
OC Euka
OC Euka
OC Mamm
OX NCBI
RN [1]
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RN [1]
RN [1]
RN ISO9
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RA Wata
RA Wata
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Best Local Similarity
Matches 190; Conserv
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Q9H8I7;
Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                       ISSUE-PLACENTA;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T.;
"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK023655; BAB14629.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDNA FLJ135ys ...
Homo sapiens (Human).
Homo sapiens (Human).
Tharyota; Metazoa; Chordata; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA FLJ13593 fis, clone PLACE1009493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                               141
201
                                      61
                   SIYSWIDTLSTRPGYLWVVWIYRNLIGSVHFFFILTLIVLIITYLYWQITEGRKIMIRLL 120
                                                                                                  MMNFQPPSKAWRASQMMTFF1F1LFFPSFTGVLCTLAITIWRLKPSADCGPFRGLPLFIH
SIYSWIDTLSTRPGYLWVVWIYRNLIGSVHFFFILTLIVLIITYLYWQITEGRKIMIRLL
                                                                               MMNFQPPSKAWRASQMMTFFIFLLFFPSFTGVLCTLAITIWRLKPSADCGPFRGLPLFIH
                                                                                                                                                                                                                                           330 AA;
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38958 MW;
                                                                                                                                                                            100.0%;
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                                                                                                                                                          Score 190; DB 4; Pred. No. 6.6e-196; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Catarrhini;
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                                                                                                                                                                                                                                         EBA21A1AC1455C2E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hominidae;
                                                                                                                                                                                               Length 330;
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anabaena

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RESULT
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ID Q9
AC Q9
AC Q9
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DT 01
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RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Flujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Mynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Havashizaki Y.,
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Best I
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01-JUN-2001 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
4932443LOBRik protein.
                                                                                                                                                                                                                                                    Q9UXT5
Q9UXT5;
01-MAY-2000
01-MAY-2000
01-JUN-2002
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EMBL; AK016573; BAB30314.1; -.
MGD; MGI:1921674; 4932443L08Rik.
SEQUENCE 757 AA; 87667 MW; 3
                                                                                Pyrococcus.
                                                                                                         Pyrococcus abyssi.
Archaea; Euryarchaeota;
                                                                                                                                                                                         PAB1174.
                                                                                                                                                                                                                        Hypothetical
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Eukaryota; Metazoa; Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y.;
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(TrEMBLrel. 17, Last sequence update)
(TrEMBLrel. 17, Last annotation update)
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4.7e-33;
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                 Q97KL3;
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01-OCT-2001
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ATPase with
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Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ248288; CAB50678.1; -.
InterPro; IPR005242; Cons_hypoth374.
Pfam; PF03706; UPF0104; 1.
TIGRFAMS; TIGR00374; TIGR00374; 1.
Hypothetical protein; Complete proteome.
SEQUENCE 335 AA; 37288 MW; F29086681DAFCFFF CRC64;
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Science 282:2012-2018(1998).
EMBL; Z81554; CAB04503.1; -.
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Rhabditidae; Peloderinae;
NCBI_TaxID=6239;
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InterPro; IPR001810; F-box.
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Heilig R.;
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xT; SM00256; FBOX; 1.
SITE; PS50181; FBOX; 1.
JENCE 351 AA; 40374 MW;
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8; Conserv
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Q95KK4;
Q1-DEC-2001 (TrEMBLrel. 19, C
01-DEC-2001 (TrEMBLrel. 19, L
01-JUN-2002 (TrEMBLrel. 21, L
Single-stranded DNA binding p
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SEQUENCE
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SIGNAL
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MEDLINE-21359325; PubMed-11466286;
Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
Tatusov R.L., Sabathe F., Districte-Stamm L., Soucaille P., Daly M.:
Bennett G.N., Koonin E.V., Smith D.R.;
"Genome sequence and comparative analysis of the solvent-producing bacterium Clostridium acetobutylicum.";
J. Bacteriol. 183:4823-4838(2001).
EMBL; AE007505; AAK78880.1; -.
                                                                                                                                            TIGREAMS; TIGRO0621; ssb; 1.
PROSITE; PS00735; SSB_1; UNKNOWN_1.
PROSITE; PS00736; SSB_2; UNKNOWN_1.
                                                                                                                                                                                                        Dufresne C., Gueride M.; "Identification and expression of cDNA and pseudogene coding rabbit mitochondrial single-strand DNA-binding protein."; Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AJ311162; CAC38115.1; -.
                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
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InterPro; IPR003959; AAA_ATPase_centr.
InterPro; IPR001270; Chaprnin_clpA/B.
Pfam; PF00004; AAA; 2.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
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Pfam; PF00436; SSB; 1.
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                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9986;
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                                             Score 7; DB 6; Pred. No. 32; 0; Mismatches
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RESULT 7
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AC Q8R2
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RC STRAIN-C57BL/6J; TISSUE-EMBRYO;
RX MEDLINE-2108560; PubMed=11217851;
RX Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Kondo S., Yamanaka I.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Kadota K., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Havashiya N., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local
              "Functional annotation of a f Nature 409:885-690(2001).
EMBL; AK013425; BAB28850.1; -HSSP; Q04887; 3ULL.
MGD; MGI:1920040; 2810480P10R
InterPro; IPR000424; SSB_prot
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Similar to single-stranded DNA binding protein.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate
Mammalia; Eutheria; Rodentia; Sciurognathi; Murida
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                       Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2810480P10RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2810480P10Rik protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=MAMMARY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 SSLVLER 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 SSLVLER 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tted (APR-2002) to the EMBL/GenBank/DDBJ
BC028648; AAH28648.1; -
NCE 148 AA; 17157 MW; E5C00016DF6BB4C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GLAND;
                                2810480P10Rik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
               SSB_protein
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Last annotation updat
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleosto Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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DT 0
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ID 016583;
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DT 01-DEC-
DT 01-DEC-
OS Caenorh
OC Eukaryo
OC Rhabdit
OX NCBI_TA
RN [1]
RP SEQUENC
RX MEDLINE
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RC STRAIN=
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RC STRAIN=
RA WATERST
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                                                                                                                                                   Q98QA6;
Q98QA6;
01-0CT-2001;
01-0CT-2001;
01-0CT-2001;
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PROSITE; P
PROSITE; P
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Direct Submission.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ EMBL; AF016662; AAB66062.1; -.
Hypothetical protein.
SEQUENCE 170 AA; 19762 MW; D6C3E6F4BEDE52I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Gattung S., Scheet P.;
"The sequence of C. elegans
Submitted (AUG-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                    Mycoplasma pulmonis.
Bacteria; Firmicutes; Bacillus/Clostridium
                                                                                                      Hypothetical MYPU_4600.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
    Mycoplasmataceae;
NCBI_TaxID=2107;
                                                                                                                                                                                                                                                                                                                                                                                                                                        133
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; PS00735; SSB_1; 1.
; PS00736; SSB_2; 1.
E 152 AA; 17319 M
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(TrEMBLrel. 18, Last sequence update)
(TrEMBLrel. 18, Last annotation update)
l protein MYPU_4600.
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                                                                                                                                                                                                                                                                                                                                                                                      62
                            Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.7%; 5c-
100.0%; Pr
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100.0%; Pr
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Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7; DB 5; Pred. No. 36; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cosmid C33C12.";
EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                          PRT;
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33;
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5. 36;
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                                                  group; Mollicutes;
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      Q8Y8Y2;
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Query Match
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Matches 7
                                          Matches
                                                                      Query Match
                                                                                                                                                                                          Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget (
Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson I
Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell H
Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
"Comparative genomics of Listeria species.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [1]
SEQUENCE
                                                                                                       EMBL; ALDYDIAL,
ListiList; LIN00754; -.
InterPro; IPR000379; Ser_estrs_site.
InterPro; IPR000379; Complete prote
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=CLIP 11262 / SEROVAR
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Nucleic Acids Res. 2
EMBL; AL445564; CAC1
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Chambaud I., Heilig R., Ferris S.,
Moszer I., Dybvig K., Wroblewski H
                                                                                                     Hypothetical protein; Comp
SEQUENCE 202 AA; 22393
                                                                                                                                                                 Science 294:849-852(2001).
EMBL; AL596166; CAC95986.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein LIN0754.
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142 IEKLIKL 148
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                                                                                                                                                                                                                                                                                                                                                                                   PubMed=11679669;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Listeriaceae; Listeria.
NCBI_TaxID=1642;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes;
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171 HDGSLDL 177
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                                         Similarity 7; Conserv
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                                          Conservative
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29:2145-2153(2001).
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el. 19, Last sequence up
el. 20, Last annotation
lin0754.
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100.0%;
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Pred. No. 38;
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6BA8C675358D167B CRC64;
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Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
Charbit A., Chetouani F., Couve E., de Daruvar A., Dehoux P.,
Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
An Entian K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
An Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
An Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
An Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
An Nordsiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
An Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
An Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
TComparative genomics of Listeria species.";
Science 294:849-852(2001).
Science 294:849-852(2001).
Science 294:849-852(2001).
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01-MAR-2002
01-JUN-2002
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Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Listeriaceae; Listeria.
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                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                  Siegers K., Entian "Genes involved in lactis 6F3.";
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MEDLINE=21537279; PubMed=11679669;
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NCBI_TaxID=1358;
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InterPro; IPR000379; Ser_estrs_site.
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FLLFFPS 102
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202 AA; 22264 MW; 37CE2E2A8872E347 CRC64;
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RESULT 14
Q48637
ID Q4863
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DT Q1-NC
CO NISG.
OS Lactc
OC Bactc
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01-DEC-2001 (TrEMBLrel. 1
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PubMed-11572479;

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Kawarabayasi Y., Hino Y., Horikawa H., Jin-no K., Takahashi M.,

Sekine M., Baba S.-I., Ankai A., Kosugi H., Hosoyama A., Fukui S.,

Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y

Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi

Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,

Oshima T., Kikuchi H.;
                                                                                                                                                                       EMBL; AP000990; BAB67612.1; -. Hypothetical protein; Complete SEQUENCE 231 AA; 26846 MW;
                                                                                                                                                                                                                                 "Complete genome sequence of an aerobic thermoacidophilic Crenarchaeon, Sulfolobus tokodaii strain7.";
DNA Res. 8:123-140(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus tokodaii.
Archaea; Crenarchaeota;
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Immonen T., Saris P.E.J.;
"Characterization of the nisFEG operon of the "Characterization of the subsp. lactis N8 strain.";
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MEDLINE=99452385; PubMed=10524754;
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Bacteria; Firmicutes;
Streptococcaceae; Laci
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NCBI_TaxID=111955;
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STRAIN-ATCC 29413;

MEDLINE-98440130; Pubmed-9767151;

Fiedler G., Arnold M., Maldener I.;

Fiedler G., Arnold M., Maldener I.;

"Sequence and mutational analysis of the devBCA general putative ABC transporter in the cyanobacterium And ATCC 29413.";

Biochim. Biophys. Acta 1375:140-143(1998).

-1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILE EMBL; AJ003195; CAA05977.1;

InterPro; IPR003593; AAA_ATPASE.

InterPro; IPR003439; ABC_transportr.

Pfam; PF000005; ABC_transportr; 1.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE-21595285; PubMed=11759840;
MEDLINE-21595285; PubMed=11759840;
Maneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Kimura Matanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura M., Matsumoto M., Matsuno A., Muraki A.,
Kishida Y., Kohara M., Matsumoto M., Takazawa M., Yamada M.,
Nakazawa M., Yamada M.,
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SMART; SM00382; AAA; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
ATP-binding; Transport.
ATP-binding; Transport.
SMOIIENCE 244 AA; 26709 MW; 785452
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050296;
01-JUN-1998
01-JUN-1998
01-JUN-2002
ATP-binding
                                                                                                                  STRAIN-PASTEUR C NO. 7120;
MEDLINE-95095923; PubMed-8002578;
Maldener I., Fiedler G., Ernst A., Fernandez-P
"Characterization of devA, a gene required for
proheterocysts in the cyanobacterium Anabaena
J. Bacteriol. 176:7543-7549(1994).
                                                                                                                                                                                                                                                                                                                                 Q57281 PRELIMINARY; PRT; 244 AA.
Q57281;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
O1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
O1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
PCC7120 DEVB, DEVC, DEVA genes, ORF2 & ORF3 (Heterocyst ABC-transporter, ATP-binding subunit).
DEVA OR ALR3712.
                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                             Fiedler G., Arnold M Submitted (AUG-1996)
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                                                                                                                                                                                                                                                                     SEQUENCE FROM
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NCBI_TaxID=1172;
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EMBL/GenBank/DDBJ
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baena variabilis
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RESULT
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DT 01
DT 01
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Best Local
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Nucleic Acids Res. 29:2145-2153(;
EMBL; AL445563; CAC13294.1; -.
MypuList; MYPU_1210; -.
MypuListical protein; Complete p.
SEQUENCE 245 AA; 28756 MW; 5.
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DNA Res. 8:205-213(2001).
-!- SIMILARITY: BELONGS TO
EMBL; x99672; CAA67987.1;
EMBL; x79672; CAA6714.1;
                                                        047800
047800;
01-JUN-1998
01-JUN-1998
01-DEC-2001
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01-0CT-2001
01-0CT-2001
 Gymnodraco acuticeps
                                       Cytochrome
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STRAIN=UAB CTIP;
MEDLINE=21267165; PubMed=11353084;
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                       CYTB.
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Moszer I., Dybvig K., Wroblewski H.,
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InterPro; IPR003593; AAA_ATPase.
InterPro; IPR003439; ABC_transportr.
Pfam; PF00005; ABC_tran; 1.
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"Complete genomic sequence of the filamentous nitrogen-fixing anabaena sp. strain PCC 7120.";
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l protein MYPU_1210.
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065045;
01-AUG-1998 (TrEMBLrel. 0
01-AUG-1998 (TrEMBLrel. 0
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Springer-Verlag Publishers (1998).

-!- FUNCTION: COMPONENT OF THE UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL COUPLED TO ATP SYNTHESIS (BY SIMILARITY).

-!- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY BOUND TO THE PROTEIN (BY SIMILARITY).

-!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B, CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.

EMBL; AF037109; AAC04790.1; -.

InterPro; IPRO00179; Cyt_b b 6.
                                                                                                                                                                                                                                                                 SB01.
PRINTS; PR00783; MINTRINSICP. ProDom; PD000295; MIP_family; TIGRFAMS; TIGR00861; MIP; 1.
                                                           -I- SIMILARITY: BELONGS TO THE MIP/AQUAPORIN EMBL; AF051202; AAC32107.1; -. HSSP; P29972; 1FQY.
                                                                                                    "Sequence-tagged-site (STS) markers of arbitrary characterization and analysis of linkage in black Genetics 149:1089-1098(1998).

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTE
                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-98278823; PubMed=9611216;
Perry D.J., Bousquet J.;
                                                                                                                                                                                                                       Picea mariana (Black spruce).
Eukaryota; Viridiplantae; Streptophyta; Eml
Spermatophyta; Coniferopsida; Coniferales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  two mitochondrial genes.";
(In) di Prisco G., Pisano E., Clarke A. (eds. FISHES OF ANTARCTICA. A BIOLOGICAL OVERVIEW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chen W.J., Bonillo C., Lecointre ( "Phylogeny of the Channichthyidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neot Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Notothenioidei; Bathydraconidae; Gymnodraco.
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                                     InterPro; IPR000425; MIP_family.
Pfam; PF00230; MIP; 1.
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PF00033; cytochrome_b_N; 1.
TE; PS00193; CYTOCHROME_B_QO;
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251 AA;
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/AQUAPORIN FAMILY
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Euteleostei; Neoteleostei;
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es; Pinaceae;
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Q8RS30
ID Q8RS3
AC Q8RS3
DT 01-JU
RO ORF5.
GN COMEN
OG Plass
OC Bacte
OX NCBI
RN [1]
RN SEQUI
RC STRA:
RA Sota
RT "Chai
RT halo;
RT halo;
RT Appl
DR EMBL
KW Plass
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01-JAN-1998
01-JAN-1998
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Q8RS30;
Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cotton M.D., Spriggs T., Artiach P., Kaine B.P., Sykes S.M., Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
                                                                                                                                                                                                                                                                                                          Archaeoglobus fulgidus.
Archaea; Euryarchaeota; Archaeoglobi;
Archaeoglobaceae; Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sota M., Endo M., Nitta K., Kawasaki H., Tsuda M.; "Characterization of a class II defective transposon carrying to acceptate dehalogenase genes from Delftia acidovorans plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORF 5
                                                                                                                                                                                                   STRAIN=VC-16 / DSM 4304 / ATCC 49558; MEDLINE=98049343; PubMed=9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             029940
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STRAIN-WHITE LEGHORN;

RC STRAIN-WHITE LEGHORN;

RA STRAIN-WHITE LEGHORN;

RA MEDLINE-99144114; PubMed-9990303;

RA Takeuchi S., Takahashi S.;

RA Takeuchi S., Takahashi S.;

RT Takeuchi S., Takahashi S.;

RT Takeuchi S., Takahashi S.;

RA POSSIBLE involvement of melanocortin 3-receptor in the regulation of adrenal gland function in the chicken.";

RE DIOCHIM. Biophys. Acta 1448:512-518(1999).

C. -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C. -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).

C. -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

DR INTERPO. IPRO00276; GPCR_Rhodpsn.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.

DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

PROSITE; PS00237; G_PROTEIN_RECEP_F1_2; 1.

G-PROTEIN_RECEP_F1_2; 1.

G-PROTEIN_RECEP_F1_2; 1.

G-PROTEIN_RECEP_F1_2; 1.
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Best Local S
Matches 7
                                                 01-NOV-1999 (TrEMBLrel. 12, C
01-NOV-1999 (TrEMBLrel. 12, L
01-MAR-2002 (TrEMBLrel. 20, La
Y94A7B.5 protein.
Y94A7B.5.
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O93259;
O1-NOV-1998 (TrEMBLrel. 08, Created)
O1-NOV-1998 (TREMBLrel. 08, Last sequence up
O1-MAR-2002 (TREMBLrel. 20, Last annotation
Melanocortin 3-receptor.
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; 1PKUULIUZ, CDPG_MGDP_dh; 1.
Pfam; PF00984; UDPG_MGDP_dh; 1.
Pfam; PF03721; UDPG_MGDP_dh_N; 1.
Hypothetical protein; Complete proteome.
Hypothetical protein; Somplete proteome.
304 AA: 35838 MW; 36D058B58C00B0B8 CRC64;
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Nature 390:364-370(1997).
EMBL; AE001084; AAB90929.1;
TIGR; AF0302; -.
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"The co
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01-NOV-1999
                                                                                                                                                                                                                                                                                Q9XXA9
                                   Caenorhabditis elegans
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Neognathae; Galliformes; Phasianidae; Phasiani
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01-JUN-1998
01-MAR-2002
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Science 282:2012-2018(1998).
EMBL; AL023856; CAA19567.1; -.
InterPro; IPR003003; 7TM_chemo2.
InterPro; IPR000168; 7TM_nematode.
Pfam; PF01604; 7tm_5; 1.
SEQUENCE 327 AA; 37108 MW; B251B168CC77BBBD
                                                                                                                                                                                                                                                                               burgdorferi.";
Nature 390:580-586(1997).
EMBL; AE001163; AAC66977.1;
TIGR; BB0619; --
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STRAIN=ATCC 35210 / B31;

MEDLINE=98065943; PubMed=9403685;

Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayt
Lathigra R., White O., Ketchum K.A., Dodson R., Hickey
Dougherty B., Tomb J.-F., Fleichmanh J., Richardson
                                                                                                                                                               Pfam; PF02272; DHHA1; 1.
Hypothetical protein; Complete
SEQUENCE 330 AA; 37377 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman Utterback R., Bowman Utterback R., McDonald L., British R., Bowman Rarland G. Fried C. Colonald L., Weidman R., Bowman Rarland G. Fried R., McDonald L., British R., Bowman Rarland G. Fried R., McDonald L., Bowman Rarland G. Fried R., McDonald L., Bowman R., Bowman R., British R., Britis
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MEDLINE=99069613; PubMed=9851916;
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InterPro; IPR001667;
Pfam; PF01368; DHH; 1
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Spirochaetaceae; Borrelia
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Q1-MAR-2002 (TrEMBLrel. 20, C)
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Q1-MAR-2002 (TrEMBLrel. 20, L)
Q1-MAR-2002 (TrEMBLrel. 20, L)
Periplasmic binding protein c
PHND OR Z5707 OR ECS5087.
Escherichia coli O157:H7.
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                                      STRAIN=0157:H7 / RIMD 0509952;

MEDLINE=21156231; PubMed=11258796;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoya Han C.-G., Ohtsubo E., Nakyama K., Murata T., Tanaka M., Tobe Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunac Kuhara S., Shiba T., Hattori M., Shinagawa H.;

"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-12.";
DNA Res. 8:11-22(2001).
                                                                                                                                                                                                                                                               "Genome sequence of enterohaemorrhagic Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                                             STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed=11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Posfai G., Bavis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
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"The smcL gene of Listeria ivanovii encodes mediates bacterial escape from the phagocytimol. Microbiol. 33:510-523(1999).
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Gonzalez-Zorn B., Dominguez-Bernal G.,
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                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN=0157:H7 / R
                                                                                                                                                                                                                                                                                                                              Apodaca J., Anantharaman T
Welch R.A., Blattner F.R.;
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                   "Complete genome structure Mesorhizobium loti.";
DNA Res. 7:331-338(2000).
                                                                                  Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M. Takeuchi C., Yamada M., Tabata S.;
                                                                                                                                                                                        STRAIN-MAFF303099;
MEDLINE-21082930; PubMed=11214968;
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Bacteria; Proteobacteria; alpha subd
Phyllobacteriaceae; Mesorhizobium.
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C STRAIN-ATCC 25586;

X MEDLINE-21886394; PubMed=11889109;

X MEDLINE-21886394; PubMed=11889109;

A Kapatral V., Anderson I., Ivanova N., Reznik G., Los T., Lykidi A Bhattacharyya A., Bartman A., Gardner W., Grechkin G., Zhu L., A Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., A Vasieva O., Chu L., Kogan Y., Chaga O., Goltsman E., Bernal A., A Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R., A Fonstein M., Kyrpides N., Overbeek R.;

T "Genome sequence and analysis of the oral bacterium Fusobacteri nucleatum strain ATCC 25586.";

L J. Bacteriol. 184:2005-2018(2002).

E EMBL; AE010582; AAL94915.1; -.
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Complete
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical cytosolic protein FN0719.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8RFH8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Complete SEQUENCE
                                                                                                                                NDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001851; Bac_inmem_transp.
InterPro; IPR001064; Crystallin.
Pfam; PF02653; BPD_transp_2; 1.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1.
                                                                       Pterygota;
Carabus.
                                                                                           Eukaryota;
                                                                                                                   Carabus abbreviatus
                                                                                                                                        NADH dehydrogenase
                                                                                                                                                                                       Q9MKL8;
                                                                                                                                                                                                  Q9MKL8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusobacterium nucleatum Bacteria; Fusobacteria;
           Prueser F.,
                         STRAIN-F;
                                    SEQUENCE FROM N.A.
                                                         NCBI_TaxID=114446;
                                                                                                        Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=76856;
  "Colonization
                                                                                                                                                                                                                                                           335
                                                                                                                                                                                                                                                                                134 LIEKLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QIINEGK 168
                                                                                                                                                                                                                                                           LIEKLIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                        Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        proteome.
344 AA;
                                                                                                                                                                                                                                                                                                                                                      proteome;
350 AA;
                                                                                Neoptera;
                                                                                           Metazoa;
                                                                                                                                        (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation updat)
ogenase subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.7%; S llarity 100.0%; Conservative 0;
            Brueckner
                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                           341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129
ckner M.,
Canary Is
                                                                                                                                                                                                                                                                                                                                                    Hypothetical
41804 MW; 2
                                                                                           Arthropoda;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36981
                                                                             irthropoda; Tracheata; Hexap
Endopterygota; Coleoptera;
                                                                                                                                                                                                                                                                                                   J.08;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (subsp. nucleatum).
Fusobacterium.
., Mossakowski D.;
Islands by Carabus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 7; DB 1; Pred. No. 66; 0; Mismatches
                                                                                                                                                                                                                                                                                                                               Score 7;
                                                                                                                                                                                                                                                                                                        Pred. No. 67
Mismatches
                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                     protein.
21A901CF46CD50D8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE4A9A22DD070150 CRC64;
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                                                                                                                                                                                                                                                                                                            DB . 67;
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                                                                                          Hexapoda;
species: evidence
                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 344;
                                                                                                                                                                                                                                                                                                                             Length 350;
                                                                               Adephaga;
                                                                                                                                                                                                                                                                                                                                                     CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                              Fusobacterium
                                                                                           Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lykidis
                                                                               Carabidae;
                                                                                                                                                                                                                                                                                                       0;
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RESULT
Q9MEG6
ID Q9
AC Q9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-VARIOUS STRAINS; TISSUE-THORAX MUSCLE;
Su Z.H., Tominaga O., Saito S., Kim C.G., Osawa S.,
Phylogeny of Tomocarabus opaculus (Coleoptera, Cai
from mitochondrial ND5 gene sequences.";
Elytra 28:13-20(2000).
-i- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+)
EMBL; AB039808; BAA92457.1; -.
EMBL; AB039804; BAA92453.1; -.
EMBL; AB039805; BAA92455.1; -.
EMBL; AB039806; BAA92457.1; -.
EMBL; AB039806; BAA92459.1; -.
EMBL; AB039806;
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                              Q9MEG6;
01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mitochondrion
Eukaryota; Meta
Pterygota; Neop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9MEG7;
01-OCT-2000 (
01-OCT-2000 (
01-MAR-2002 (
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SEQUENCE
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                                                                                                                                              Q9MEG6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9MEG7
    NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=118064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carabus opaculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      different character complexes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157
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                                                                                                                                                                                                                                                                                   FIFLLFF
                                                                                                                                                                                                                                                                                                                                                                                         Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 3.7%;
Similarity 100.0%;
7; Conservative (
0 (TrEMBLrel. 15, () (TrEMBLrel. 15, I) 2 (TrEMBLrel. 20, I) cogenase subunit 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 AA;
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                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                     26
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Lrel. 15, Last sequence update)
Lrel. 20, Last annotation updat
subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40947
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       G
  Created)
Last sequence update)
Last annotation updat
5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                   Score 7;
Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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68;
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                                 update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Casale
                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        beetles (Proceedings
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Carabidae) as
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Best Local S
Matches 7
               Query Match
     Best Local Similarity
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Q9MEC7;
Q9MEC7;
Q9MEC7;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-MAR-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; l
Pterygota; l
                                                     EMBL; AB041069; BAA94628.1; -.
EMBL; AF219473; AAF62460.1; -.
InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
                                                                                                                                                                                           STRAIN-55; TISSUE-THORAX MUSCLE;
MEDLINE-20296815; PubMed-10835484;
MEDLINE-20296815; PubMed-10835484;
Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;
"Formation of the Japanese Carabina Fauna inferred from a phylogenetic tree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae).";
J. Mol. Evol. 50:541-549(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB039809; BAA92458.1; -.
EMBL; AB039807; BAA92456.1; -.
InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
Mitochondrion; NAD; Oxidoreductas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                    "Incongruence of mitochondrial and beetles Ohomopterus.";
Syst. Biol. 0:0-0(2000).
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                         Carabus granulatus
                                                                                                                                                                                                                                                                                                                                                            NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=118064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carabus opaculus
                                                                                                                                                       Sota T., Vogler A.P.;
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                   NCBI_TaxID=118799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       157
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                                                                                                           - CATALYTIC ACTIVITY: NADH + UBIQUINONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FIFLLFF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 100 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       355 AA;
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                                                                                                                                                                                                                                                                                                                   Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Metazoa;
                                     AA;
                                                                                                                                                                                                                                                                                                                                                          rel. 15, Created)
rel. 15, Last sequence update)
rel. 20, Last annotation update)
subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                      Arthropoda; Tracheata; Hexapoda; Insecta; Endopterygota; Coleoptera; Adephaga; Carabidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40961 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase; Ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arthropoda; Tracheata; Hexapoda; Inseq; Endopterygota; Coleoptera; Adephaga;
                                     40873 MW;
    3.7%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-THORAX MUSCLE;
aito S., Kim C.G., Osawa
us opaculus (Coleoptera,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 7; u
    Score 7; |
Pred. No.
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                                    1AFA4B4EA9BA16BA CRC64;
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                                                                                                                                            nuclear
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. 68;
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DB (
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                                                                                                           NAD(+) +
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             Length 355;
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                                                                                                            UBIQUINOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Insecta;
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                                                                                                                                            the carabid
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Best Local
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=37, 33, 34, AND 36; TISSUE=THORAX MUSCLE;

STRAIN=37, 33, 34, AND 36; TISSUE=THORAX MUSCLE;

Kim C.G., Tominaga O., Su Z.H., Osawa S.;

Norigin and Diversification of Euleptocarabus porrecticollis

"Origin and Diversification of Euleptocarabus porrecticollis"

"Origin and Diversification of Euleptocarabus porrecticollis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9ME14;
01-OCT-2000
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01-MAR-2002
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01-OCT-2000
01-MAR-2002
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Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.

STRALN=35, 31, 33, 36, AND 34; TISSUE=THORAX MUSCLE;

MEDLINE=20296815; PubMed=10835484;

Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;

"Formation of the Japanese Carabina Fauna inferred from a phylotree of mitochondrial ND5 gene sequences (Coleoptera, Carabidae J. Mol. Evol. 50:541-549(2000).

-!- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ND5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AB041059; BAA94618.1; -. EMBL; AB041054; BAA94613.1; -. EMBL; AB041056; BAA94615.1; -. EMBL; AB041057; BAA94616.1; -. EMBL; AB041058; BAA94617.1; -.
                                                                                                                                                                                                                                                                                                                                                       Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001750 Pfam; PF00361; oxide Mitochondrion; NAD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9ME44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                  NCBI_TaxID=87295;
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Neoptera;
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                                                                                                                                                                                                                                                                                                                                                             Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                               Metazoa;
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Endopterygota; Coleoptera; Adepl
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Last annotation updat
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Pred. No. 68;
0; Mismatches
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ota; Coleoptera; Adephaga; Car
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(Coleoptera, Carabidae).";
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RESULT
Q9MDT2
ID Q9
AC Q9
AC Q9
DT 011
DT 01
DT 01
DT 01
DT NE
GN NE
GN NE
OG MI
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Q9MDZ5
ID Q9
AC Q9MDZ5
DT 01

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Matches 7
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Best Local 9
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                                                                                                     Q9MDT2;
01-OCT-2000
01-OCT-2000
01-MAR-2002
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01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
Mitochondrion; NAD; Oxidoreductase;
NON_TER 1 1
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EMBL; AB022586; BAA74498.1; --
EMBL; AB022587; BAA74499.1; --
EMBL; AB022589; BAA74501.1; --
                      Mitochondri
                                                                                NADH dehydrogenase
                                                                                                                                                                                      Q9MDT2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carabus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9MDZ5
                                        Carabus porrecticollis kansaiensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=118064;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carabus opaculus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NADH dehydrogenase
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                                                                                                                                                                                                                                                                                        |||||||
| FIELLEF 163
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                                                                                                                                                                                                                                                                                                                                                                     Similarity 7; Conserv
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(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
ogenase subunit 5 (Fragment).
                                                                             (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last sequence update)
(TrEMBLrel. 20, Last annotation updat)
ogenase subunit 5 (Fragment).
                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                      Conservative
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TIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arthropoda; Tracheata; Hexapoda; Insecta; Endopterygota; Coleoptera; Adephaga; Carabidae;
Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40914 MW;
                                                                                                                                                                                                                                                                                                                                                               3.,
100.0%; F,
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    40899 MW;
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                                                                                                                                                                                                                                                                                                                                                                   Score 7; DB 8; Pred. No. 68; 0; Mismatches
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Pred. No.
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                                                                                                                                                                                    PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67A294D3AE3C4B30 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  704B4C5FBCA13D00 CRC64;
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                                                                                                                                                                                    AA.
                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                         Length 355;
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                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT
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Best Local S
Matches 7
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Best Local S
Matches 7
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=45, 43, AND 39; TISSUE-THORAX MUSCLE;

STRAIN=45, 43, AND 39; TISSUE-THORAX MUSCLE;

MEDLINE-20296815; PubMed=10835484;

Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;

Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;

"Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina Fauna inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the Japanese Carabina" inferred from a phylogenetic "Formation of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tree of mitochondrial ND5 gene sequences (Coleoptera, J. Mol. Evol. 50:541-549(2000).
-:- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(+) + 1 EMBL; AB041073; BAA94632.1; -. EMBL; AB041070; BAA94629.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota;
Pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AB022576; BAA74488.1; -.
EMBL; AB022575; BAA74487.1; -.
InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
Mitochondrion; NAD; Oxidoreductase;
NON_TER 1 1
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01-OCT-2000 (TrEMBLrel. 15, L
01-MAR-2002 (TrEMBLrel. 20, L
NADH dehydrogenase subunit 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Coleoptera, Carabidae) in the Japanese Islands Mitochondrial ND5 Gene Sequences."; Mol. Phylogenet. Evol. 0:0-0(1999).
-i- CATALYTIC ACTIVITY: NADH + UBIQUINONE - NAD(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-23, AND 22; TISSUE-THORAX MUSCLE; Kim C.G., Tominaga O., Su Z.H., Osawa S., "Origin and Diversification of Euleptocarabus
                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB041071;
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157 FIFLLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                157 FIFLLFF 163
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                                                                                   20 FIFLLFF 26
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                                                                                                                                                                       Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                          355 AA;
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Conservative
163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAA94630.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arthropoda; Tracheata; Hexapoda; Insecta; ; Endopterygota; Coleoptera; Adephaga; Carabidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40944 MW;
                                                                                                                                                                                                                                                                                                                                                          40803 MW;
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                          8BC0FEE5FFB605A0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UBIQUINONE - NAD(+) + UBIQUINOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8A2E3165B68D5F10 CRC64;
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RESULT Q9MDS6

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Best Local S
Matches 7
SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=49, AND 47; TISSUE-THORAX MUSCLE;

STRAIN=20296815; PubMed=10835484;

MEDLINE=20296815; PubMed=10835484;

Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., (
"Formation of the Japanese Carabina Fauna inferred from tree of mitochondrial ND5 gene sequences (Coleoptera, J. Mol. Evol. 50:541-549(2000).

J. Mol. Evol. 50:541-549(2000).
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01-OCT-2000 (
01-MAR-2002 (
                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; I Pterygota; Neoptera;
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Mol. Phylogenet. Evol. 0:0-0(1999).
-!- CATALYTIC ACTIVITY: NADH + UBIQ
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01-MAR-2002
                                                                                                                                                                                                                                                                                    NCBI_TaxID=118799;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kim C.G., Tominaga O., Su Z.H., Osawa S.;
"Origin and Diversification of Euleptocarabus
(Coleoptera, Carabidae) in the Japanese Island
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=VARIOUS STRAINS;
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|FIFLLFF 163
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PF00361; oxidored_q1; 1.
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BLrel. 20,
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Lrel. 15, Last sequence
Lrel. 20, Last annotat
subunit 5 (Fragment).
                                                                                                                                                                                                                                                                                                                                       Arthropoda; Tracheata; Hexapoda; Inseq
; Endopterygota; Coleoptera; Adephaga;
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Endopterygota; Coleoptera; Adephaga; Carabidae;
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                                                                                             , Imura Y., Os.
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                           NAD(+) + UBIQUINOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 355;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                Insecta;
                                                                              Osawa S.;
om a phylogenetic
Carabidae).";
                                                                                                                                                                                                                                                                                                                                          Carabidae;
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RESULT
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AC Q9
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Q9MDR4
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Best Local S
Matches 7
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Best Local S
Matches 7
                                                                                                                                                                  Q9MDR3
Q9MDR3;
Q1-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Os "Formation of the Japanese Carabina Fauna inferred from tree of mitochondrial ND5 gene sequences (Coleoptera, Ca J. Mol. Evol. 50:541-549(2000).

-i- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBI EMBL; AB041084; BAA94643.1; -
EMBL; AB041083; BAA94642.1; -
InterPro; IPR001750; Oxidored_q1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB041067; BAA94626.1; -.
EMBL; AB041066; BAA94625.1; -.
InterPro; IPR001750; Oxidored_q1.
Pfam; PF00361; oxidored_q1; 1.
Mitochondrion; NAD; Oxidoreductase; Ubiquinone.
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001750; Oxidore Pfam; PF00361; Oxidored_q1; Mitochondrion; NAD; Oxidore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence up
01-MAR-2002 (TrEMBLrel. 20, Last annotation
NADH dehydrogenase subunit 5 (Fragment).
 Carabus.
NCBI_TaxID=120935;
                                         Pterygota;
                                                             Eukaryota;
                                                                                                       Carabus schrencki.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE-THORAX MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pterygota;
Carabus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carabus munakatai.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                     Mitochondrion.
                                                                                                                                              NADH dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20296815;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=120937;
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                                         Metazoa; I Neoptera;
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0 (TrEMBLrel. 15, L:
2 (TrEMBLrel. 20, L:
rogenase subunit 5
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                                                                                                                                                                                                                                                       PRELIMINARY;
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.H., Kim C.G., Okamoto
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                                         Arthropoda; Tracheata; Hexapoda; Insecta;
; Endopterygota; Coleoptera; Adephaga; Carabidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Ubiquinone.
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100.0%;
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Last annotation updat
5 (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred.
                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 956C1181F08A06FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                           red. No. 68;
Mismatches
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68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8;
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                                                                                                                                                                   update)
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om a phylogenetic
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RP SEQUENCE FROM N.A.

RC TISSUE-THORAX MUSCLE;

RC TISSUE-THORAX MUSCLE;

RX MEDLINE-20296815; PubMed=10835484;

RA Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;

RA Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;

RA Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;

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RA Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;

RA Tominaga O., Su Z.H., Kim C.G., Okamoto M., Imura Y., Osawa S.;

RA Tominaga O., Su Z.H., Kim
                                                                                                                                                                                                                                                                                                         RESULT
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Matches 7
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Best Local S
Matches 7
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01-OCT-2000
01-OCT-2000
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.

STRAIN=12, 1, 2, 3, 4, 5, 6, 9, 10, AND 11; TISSUE=THORAX MUSTRAIN=12, 1, 2, 3, 4, 5, 6, 9, 10, AND 11; TISSUE=THORAX MUSTRAIN=12, 1, 70 and 5 and 5
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EMBL;
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EMBL;
EMBL;
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Pfam; PF00361;
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                                                                                                                                                                                                                                                                                                                                                                                     Mitochondrion; NAD;
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   157
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                                                                      FIFLLFF 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||||
|FIFLLFF 163
   FIFLLFF
                                                                                                                                                  Similarity 7; Conserv
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7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neoptera;
                                                                                                                                                                                                                                                                                                            355 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Tremblrel. 15, Created)
(Tremblrel. 15, Last sequence update)
(Tremblrel. 20, Last annotation updato)
ogenase subunit 5 (Fragment).
                                                                                                                                                      Conservative
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   163
                                                                                                                                                                                                                                                                                                                                                                                                                          01750; Oxidored_q1.
oxidored_q1; 1.
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                                                                                                                                                                                                                                                                                                                                                                               Oxidoreductase; Ubiquinone.
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100.0%; Pr
                                                                                                                                                                                                                                                                                                     40916 MW;
                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                   3.7%;
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                                                                                                                                                                                       Score 7;
Pred. No
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                         E6B39DF6723A8FEB
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                          No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355
                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11; TISSUE-THORAX MUSCLE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAD(+) + UBIQUINOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                            Length 355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 355;
                                                                                                                                                                                                                                                                                                         CRC64;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                               Gaps
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Search completed: November Job time: 95 secs

9

2002,

07:30:24

0

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RESULT 45
Q9MDB8
AC Q9MDB
AC Q9MDB
DT 01-OC
DT 01-M
DE NADH
GN ND5.
OS Cara
OG Mito
OC Euka
OC Pter
OC Care
OC STR
RA SU
RA SU
RT frc
RL Ely
CC -1:
DR EMI
DR Pf
KW M1
DR Pf
KW M1
SEQ
SE
뮹
                           Ş
                                                                        Query Match
Best Local
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9MDB8;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 20, Last annotation updat
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
NADH dehydrogenase subunit 5 (Fragment).
                                                                                                                                           STRAIN-HOKKAIDO-KUSHIRO2, AND HOKKAIDO-NEMURO1; TISSUE-THORAX MUSCLE; Su Z.H., Tominaga O., Saito S., Kim C.G., Osawa S.; Su Z.H., Tominaga O., Saito S., Kim C.G., Osawa S.; Phylogeny of Tomocarabus opaculus (Coleoptera, Carabidae) as deduced from mitochondrial ND5 gene sequences."; Elytra 28:13-20(2000).

Elytra 28:13-20(2000).

-1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+) + UBIQUINOL.

EMBL; AB039794; BAA92444.1; -.

EMBL; AB039794; BAA92443.1; -.

InterPro; IPR001750; Oxidored_q1.

Pfam; PF00361; oxidored_q1; 1.

Mitochondrion; NAD; Oxidored_q1; 1.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; l
Pterygota;
                                                                                                                     Mitochondrion; | NON_TER 1 | SEQUENCE 355 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9MDB8
                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=118064;
                                                                                                                                                                                                                                                                                                                                                                   Carabus
                                                                                                                                                                                                                                                                                                                                                                                                              Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                         Carabus opaculus.
157
                             20 FIFLLFF 26
FIFLLFF
                                                        Similarity 7; Conserv
                                                                                                                    355 AA;
                                                                                                                                                                                                                                                                                                                                                                               Neoptera;
                                                                                                                                                                                                                                                                                                                                                                                              Metazoa;
                                                           Conservative
163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                              Arthropoda; Tracheata; Hexapoda; Insecta; ; Endopterygota; Coleoptera; Adephaga; Carabidae;
                                                                                                                     40959 MW;
                                                                       3.7%;
                                                           0;
                                                                        Score 7; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                     F071F1D770E4FED4 CRC64;
                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   355
                                                                           DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                    Length 355
                                                           0;
                                                           Indels
                                                           0;
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